APS
8/4/98
08/8/19,681

```
Trying 01181...Open

Connection closed by remote host

Timed out

The modem is not responding to modem commands.

Trying 01082...Open

PLEASE ENTER HOST PORT ID:
PLEASE ENTER HOST PORT ID:x
LOGINID:d186tmc
PASSWORD:
TERMINAL (ENTER 1, 2, 3, 4, OR ?):3


 * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
 *                                                                     *
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 *       * PLEASE USE 305-9000 FOR NEW TELEPHONE NUMBER *              *
 *                                                                     *
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 * More U.S. patent data is now available on APS.  The new            *
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 *  DISCLAIMER:                                                        *
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 *  such, of the data.                                                 *
 * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
 *                Help Desk --> 703-305-9000                           *
 *                                                                     *
 *    The Help Desk is staffed for APS support 7 days/week.            *
 *      Monday through Friday:      6:30am - 9:00pm                    *
 *      Saturday, Sunday, Holidays: 8:30am - 5:00 pm                   *
 *                                                                     *
 *    The Help Desk staff at this number will handle all APS           *
 *    related questions.                                               *
 * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
 *    >>>>>>>>>>>>> NEW SUNDAY HOURS !!! <<<<<<<<<<<<<                 *
 *                                                                     *
 *    The APS is available:                                            *
 *            6:30am - 9:00pm Monday through Friday                    *
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  *           7:30am - 5:00pm Saturday, Sunday, Holidays          *
  *                                                               *
  *      APS is unavailable Thanksgiving Day, Christmas Day,      *
  *      and New Year's Day.                                      *
  *                                                               *
  * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
FILE 'USPAT' ENTERED AT 08:59:28 ON 04 AUG 1998

  * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
  *              W E L C O M E   T O   T H E                      *
  *         U. S.   P A T E N T   T E X T   F I L E               *
  * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

=> s MAGE-1

           196 MAGE
       2323337 1
L1          41 MAGE-1
                (MAGE(W)1)

=> s l1 and MAGE?/clm

          4227 MAGE?/CLM
L2          13 L1 AND MAGE?/CLM

=> t l2/3/1-13

'L2' MUST END IN '/Q', '/A', OR '/L'

=> t l2 1-12
```

1. 5,763,165, Jun. 9, 1998, Method for determining lung adenocarcinomas by assaying for one or more of **MAGE-1**, MAGE-2 and MAGE-3; Thierry Boon-Falleur, et al., 435/6, 91.2 [IMAGE AVAILABLE]

2. 5,763,155, Jun. 9, 1998, Method for determining lung adenocarcinomas by assaying for one or more of **MAGE-1**, MAGE-2 and MAGE-3 gene products; Thierry Boon-Falleur, et al., 435/4, 7.1, 7.23 [IMAGE AVAILABLE]

3. 5,759,783, Jun. 2, 1998, Method of screening for cancer by detecting messenger RNA for a MAGE-XP gene; Christophe Lurquin, et al., 435/6, 91.2; 536/24.33 [IMAGE AVAILABLE]

4. 5,662,907, Sep. 2, 1997, Induction of anti-tumor cytotoxic T lymphocytes in humans using synthetic peptide epitopes; Ralph T. Kubo, et al., 424/195.1, 193.1, 197.11, 277.1; 530/300, 328, 403 [IMAGE AVAILABLE]

5. 5,629,166, May 13, 1997, Method for identifying individuals suffering from a cellular abnormality some of whose abnormal cells present complexes of HLA-C-clone 10/**MAGE-1** derived peptides, and methods for treating said individuals; Pierre van der Bruggen, et al., 435/7.23, 6, 7.21; 436/64 [IMAGE AVAILABLE]

6. 5,612,201, Mar. 18, 1997, Isolated nucleic acid molecules useful in determining expression of a tumor rejection antigen precursor; Etienne De Plaen, et al., 435/91.2, 6; 536/23.1, 24.33 [IMAGE AVAILABLE]

7. 5,610,013, Mar. 11, 1997, Method for diagnosing a disorder by determining expression of gage tumor rejection antigen precursors; Benoit Van den Eynde, et al., 435/6, 7.1, 252.3, 252.33, 320.1, 325, 358, 362, 365; 536/23.5 [IMAGE AVAILABLE]

8. 5,587,289, Dec. 24, 1996, Isolated nucleic acid molecules which are members of the MAGE-Xp family and uses thereof; Christophe Lurquin, et

al., 435/6, 252.3, 320.1, 325; 536/23.1 [IMAGE AVAILABLE]

9. 5,571,711, Nov. 5, 1996, Isolated nucleic acid molecules coding for BAGE tumor rejection antigen precursors; Pierre van der Bruggen, et al., 435/365, 69.3, 172.3, 252.3, 320.1; 536/23.5; 935/9, 32, 34, 55, 57, 70, 71 [IMAGE AVAILABLE]

10. 5,541,104, Jul. 30, 1996, Monoclonal antibodies which bind to tumor rejection antigen precursor **mage-1**; Yao-Tseng Chen, et al., 435/344.1; 424/138.1, 155.1, 174.1; 435/69.6, 70.21, 172.2; 530/350, 387.7, 388.8; 935/15 [IMAGE AVAILABLE]

11. 5,512,444, Apr. 30, 1996, Method for determining bladder tumors by assaying for MAGE-1,2,3 or 4; Jean-Jacques Patard, et al., 435/6, 7.1, 7.9, 91.2; 536/23.1, 24.3 [IMAGE AVAILABLE]

12. 5,512,437, Apr. 30, 1996, Method for determining head and neck squamous cell carcinomas, prostate carcinomas, and bladder tumors by assaying for mage-3; Beatrice Gaugler, et al., 435/6, 7.1, 7.9, 91.2; 536/23.1, 24.3 [IMAGE AVAILABLE]

=> t 1-12 clm

US PAT NO: 5,763,165 [IMAGE AVAILABLE] L2: 1 of 13

CLAIMS:

CLMS(1)

We claim:

1. Method for screening a sample of lung tissue for possible presence of adenocarcinoma, comprising assaying said sample and determining expression of a gene which codes for a tumor rejection antigen precursor selected from the group consisting of **MAGE-1**, **MAGE**-2 and **MAGE**-3, wherein expression of said gene is an indication of possible presence of adenocarcinoma in said sample.

CLMS(2)

2. The method of claim 1, comprising determining expression of said tumor rejection antigen precursor via nucleic acid molecule amplification.

CLMS(3)

3. The method of claim 1, comprising determining expression of said tumor rejection antigen precursor via polymerase chain reaction.

CLMS(4)

4. The method of claim 1, comprising determining expression of said tumor rejection antigen precursor via a labelled nucleotide probe which specifically hybridizes to a sequence coding for said tumor rejection antigen precursor.

CLMS(5)

5. The method of claim 3, wherein said polymerase chain reaction is carried out with at least one nucleotide primer selected from the group consisting of SEQ ID NO: 1 and SEQ ID NO: 2.

CLMS(6)

6. The method of claim 3, wherein said polymerase chain reaction is

carried out with at least one nucleotide primer selected from the group consisting of SEQ ID [redacted] 3 and SEQ ID NO: 4.

CLMS(7)

7. The method of claim 3, wherein said polymerase chain reaction is carried out with at least one nucleotide primer selected from the group consisting of SEQ ID NO: 5 and SEQ ID NO: 6.

CLMS(8)

8. The method of claim 4, wherein said labelled nucleotide probe consists of labelled SEQ ID NO: 1 or labelled SEQ ID NO: 2.

CLMS(9)

9. The method of claim 4, wherein said radiolabelled nucleotide probe consists of SEQ ID NO: 3 or SEQ ID NO: 4.

CLMS(10)

10. The method of claim 4, wherein said labelled nucleotide probe consists of labelled SEQ ID NO: 5 or labelled SEQ ID NO: 6.

CLMS(11)

11. Method for determining presence or amount of expression of a tumor rejection antigen precursor selected from the group consisting of **MAGE-1**, **MAGE**-2 and **MAGE**-3 in a lung adenocarcinoma, comprising contacting said sample with an agent which reacts with a nucleic acid molecule coding for said tumor rejection antigen precursor or an expression product of said gene, and determining reaction of said agent as a determination of presence or amount of said tumor rejection antigen precursor.

US PAT NO: 5,763,155 [IMAGE AVAILABLE] L2: 2 of 13

CLAIMS:

CLMS(1)

We claim:

1. A method for screening a sample of lung tissue for possible presence of adenocarcinoma, comprising assaying said sample and determining an expression product of a gene which codes for a tumor rejection antigen precursor selected from the group consisting of **MAGE-1**, **MAGE**-2, and **MAGE**-3, wherein said expression product of said gene is an indication of possible presence of adenocarcinoma in said sample.

CLMS(2)

2. The method of claim 1 comprising determining said expression product via an immunoassay.

US PAT NO: 5,759,783 [IMAGE AVAILABLE] L2: 3 of 13

CLAIMS:

CLMS(1)

We claim:

1. Method for screening for possibility of a, non-small cell lung carcinoma, melanoma, breast cancer, sarcoma or leukemia in a nucleic acid-containing sample taken from a human, comprising contacting said

sample with at least one nucleic acid molecule which hybridizes to mRNA or cDNA corresponding to an **MAGE**-Xp gene, and determining hybridization to said mRNA or cDNA as a determination of possible presence of non-small cell lung carcinoma, melanoma, breast cancer, sarcoma or leukemia in said sample.

CLMS(2)

2. The method of claim 1, wherein said **MAGE**-Xp gene is **MAGE**-Xp2.

CLMS(3)

3. The method of claim 2, comprising contacting said sample with (a) SEQ ID NO: 5 and SEQ ID NO: 6, (b) SEQ ID NO: 7 and SEQ ID NO: 8, or (c) SEQ ID NO: 9 and SEQ ID NO: 10.

CLMS(4)

4. The method of claim 3, comprising contacting said sample with SEQ ID NO: 5 and SEQ ID NO: 6.

CLMS(5)

5. The method of claim 1, further comprising carrying out a polymerase chain reaction following said hybridization.

CLMS(6)

6. The method of claim 5, wherein said polymerase chain reaction comprises contact with at least two nucleic acid primers.

US PAT NO: 5,662,907 [IMAGE AVAILABLE] L2: 4 of 13

CLAIMS:

CLMS(1)

What is claimed is:

1. A composition comprising: a helper peptide having a T helper epitope, and an immunogenic peptide having the sequence EVDPIGHLY (SEQ. ID. No.2).

CLMS(2)

2. A pharmaceutical composition comprising: a pharmaceutically acceptable carrier, a helper peptide comprising a T helper epitope, and an immunogenic peptide having the sequence EVDPIGHLY (SEQ. ID. NO.2).

CLMS(3)

3. The composition of claim 2, further comprising an adjuvant.

CLMS(4)

4. The method of claim 3, wherein the adjuvant is incomplete Freund's adjuvant.

CLMS(5)

5. The method of claim 3, wherein the adjuvant is Seppic Montanide ISA-51.

CLMS(6)

6. The composition of claim 2, wherein the helper peptide is lipidated.

CLMS(7)

7. The composition of claim 6, wherein the lipid is palmitic acid.

CLMS(8)

8. The composition of claim 6, wherein the T helper epitope is QYIKANSKFIGITE (SEQ ID NO.:5).

CLMS(9)

9. The composition of claim 6, wherein the T helper epitope is aKXVWANTLKAAa (SEQ ID NO.:10).

CLMS(10)

10. The composition of claim 2, wherein the helper peptide comprising a T helper epitope and the immunogenic peptide having the sequence EVDPIGHLY (SEQ ID NO:2) are linked.

CLMS(11)

11. The composition of claim 10, wherein the T helper epitope is QYIKANSKFIGITE (SEQ ID NO.:5).

CLMS(12)

12. The composition of claim 10, wherein the T helper epitope is aKXVWANTLKAAa (SEQ ID NO.:10).

CLMS(13)

13. The method of inducing an immune response against a target tumor cell expressing an HLA-A1 molecule and a **MAGE**-3 protein, the method comprising contacting cytotoxic T cell with an immunogenic peptide having the sequence EVDPIGHLY (SEQ. ID. No.2) under conditions that induce a cytotoxic T cell response against the target cell.

CLMS(14)

14. The method of claim 13, wherein the cytotoxic T cells are contacted with the immunogenic peptide in vitro.

CLMS(15)

15. A method of inducing an immune response against a **MAGE**-3-expressing tumor cell in a patient having an HLA-A1 allele, the method comprising repetitively administering to the patient a composition comprising an equimolar mixture of an immunogenic peptide having a sequence EVDPIGHLY (SEQ ID No:2) and a peptide having a sequence aKXVWANTLKAAa (SEQ ID No:10) in an amount to induce the immune response.

CLMS(16)

16. The method of claim 15, wherein the composition is administered at least five times.

CLMS(17)

17. The method of claim 15, wherein the composition is administered at least ten times.

CLMS(18)

18. The method of claim 13, further comprising contacting the cytotoxic T cells with a peptide comprising a T helper epitope.

CLMS(19)

19. The method of claim 18, wherein the peptide comprising a T helper epitope is lipidated.

CLMS(20)

20. The method of claim 19, wherein the lipid is palmitic acid.

CLMS(21)

21. The method of claim 18, wherein the T helper epitope is QYIKANSKFIGITE (SEQ ID NO:5).

CLMS(22)

22. The method of claim 18, wherein the T helper epitope is aKXVWANTLKAAa (SEQ ID NO:10).

CLMS(23)

23. The method of claim 18, wherein the immunogenic peptide is linked to the peptide comprising a T helper epitope.

US PAT NO: 5,629,166 [IMAGE AVAILABLE] L2: 5 of 13

CLAIMS:

CLMS(1)

We claim:

1. Method for determining cancer in a subject having malignant cells which present complexes of HLA-C clone 10 and **MAGE-1** derived peptides on their surfaces, comprising contacting a CTL containing sample taken from a subject suspected of having cancer with cells which express both (i) molecules of HLA-C clone 10 and (ii) molecules of **MAGE-1**, and determining at least one of proliferation of cytolytic T cells in said CTL containing sample or lysis of said cells which express both (i) molecules of HLA-C clone 10 and (ii) molecules of a **MAGE-1** gene to determine presence of cytolytic T cells which specifically bind complexes of HLA-C clone 10 and a **MAGE-1** derived peptide as a determination that said subject has cancer.

CLMS(2)

2. The method of claim 1, wherein said cells which express both (i) molecules of HLA-C clone 10 and (ii) molecules of **MAGE-1** are transfectants.

CLMS(3)

3. The method of claim 1, wherein said cells which express both (i) molecules of HLA-C clone 10 and (ii) molecules of **MAGE-1** have been transfected with at least one of (i) a nucleic acid molecule which codes for HLA-C-clone 10 and (ii) a nucleic acid molecule which codes for tumor rejection antigen precursor **MAGE-1**.

CLMS(4)

4. The method of claim 1, wherein said cells which express both (i) molecules of HLA-C clone 10 and (ii) molecules of **MAGE-1** have been transfected with both (i) a nucleic acid molecule which codes for HLA-C-clone 10 and (ii) a nucleic acid molecule which codes for tumor rejection antigen precursor **MAGE-1**.

CLMS(5)

5. The method of claim 3, wherein said transfected cells are COS cells.

CLMS(6)

6. The method of claim 1, comprising determining proliferation of said cytolytic T cells via determining tumor necrosis factor release by said cytolytic T cells.

CLMS(7)

7. The method of claim 1, comprising determining lysis of said cells which express both (i) molecules of HLA-C clone 10 and (ii) molecules of **MAGE-1** via a .sup.51 Cr chromium release assay.

US PAT NO: 5,612,201 [IMAGE AVAILABLE] L2: 6 of 13

CLAIMS:

CLMS(1)

We claim:

1. Isolated nucleic acid molecule selected from the group consisting of: SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, and SEQ ID NO: 46.

CLMS(2)

2. Kit useful in determining expression of a **MAGE** gene, said kit comprising at least one pair of primers selected from the group consisting:
(b) SEQ ID NO: 29 and SEQ ID NO: 30
(c) SEQ ID NO: 31 and SEQ ID NO: 32
(d) SEQ ID NO: 33 and SEQ ID NO: 34
(e) SEQ ID NO: 35 and SEQ ID NO: 36
(f) SEQ ID NO: 37 and SEQ ID NO: 38
(g) SEQ ID NO: 39 and SEQ ID NO: 40
(h) SEQ ID NO: 41 and SEQ ID NO: 42
(i) SEQ ID NO: 43 and SEQ ID NO: 44 and
(j) SEQ ID NO: 45 and SEQ ID NO: 46.

CLMS(3)

3. Method for determining expression of a **MAGE** gene of interest, comprising contacting a nucleic acid containing sample with at least one pair of primers selected from the group consisting:
(b) SEQ ID NO: 29 and SEQ ID NO: 30
(c) SEQ ID NO: 31 and SEQ ID NO: 32
(d) SEQ ID NO: 33 and SEQ ID NO: 34
(e) SEQ ID NO: 35 and SEQ ID NO: 36
(f) SEQ ID NO: 37 and SEQ ID NO: 38
(g) SEQ ID NO: 39 and SEQ ID NO: 40
(h) SEQ ID NO: 41 and SEQ ID NO: 42
(i) SEQ ID NO: 43 and SEQ ID NO: 44 and
(j) SEQ ID NO: 45 and SEQ ID NO: 46, subjecting said nucleic acid containing sample and pair of primers to a reverse transcriptase-polymerase chain reaction, and determining any amplification product as a determination of expression of said **MAGE** gene.

US PAT NO: 5,610,013 [IMAGE AVAILABLE] L2: 7 of 13

CLAIMS:

CLMS(1)

We claim:

1. Method for screening for a disorder characterized by expression of a GAGE tumor rejection antigen precursor, comprising contacting a sample which does not contain normal testes cells from a subject believed to have said disorder, with a probe which hybridizes to a cDNA or mRNA molecule which codes for said GAGE tumor rejection antigen precursor, and determining hybridization of said probe to said cDNA or mRNA, wherein said hybridization is an indication of said disorder in said subject.

CLMS(2)

2. Method for screening for a disorder characterized by expression of a tumor rejection antigen precursor coded for by a cDNA molecule comprising nucleotides 51-476 of SEQ ID NO: 1, comprising contacting a sample from a subject believed to suffer from said disorder with an antibody specific for an expression product of SEQ ID NO: 1, and determining binding between said antibody and said expression product as an indication of possible presence of said disorder in said subject.

CLMS(3)

3. The method of claim 1, wherein said disorder is melanoma.

CLMS(4)

4. The method of claim 2, wherein said disorder is melanoma.

CLMS(5)

5. The method of claim 1, wherein said disorder is breast cancer.

CLMS(6)

6. The method of claim 2, wherein said disorder is breast cancer.

CLMS(7)

7. The method of claim 1, wherein said disorder is a larynx or pharynx tumor.

CLMS(8)

8. The method of claim 2, wherein said disorder is a larynx or pharynx tumor.

CLMS(9)

9. The method of claim 1, wherein said disorder is sarcoma.

CLMS(10)

10. The method of claim 2, wherein said disorder is sarcoma.

CLMS(11)

11. The method of claim 1, wherein said disorder is bladder cancer.

CLMS(12)

12. The method of claim 2, wherein said disorder is bladder cancer.

CLMS(13)

13. The method of claim 1, wherein said disorder is colon carcinoma.

CLMS(14)

14. The method of claim 2, wherein said disorder is colon carcinoma.

CLMS(15)

15. Isolated nucleic acid molecule selected from the group consisting of SEQ ID NO: 2 and SEQ ID NO: 3.

CLMS(16)

16. An isolated nucleic acid molecule consisting of the nucleotide sequence set forth in SEQ ID NO: 1.

CLMS(17)

17. An isolated nucleic acid molecule, the complementary sequence which hybridizes, under stringent conditions, to the nucleic acid molecule set forth in SEQ ID NO: 1, and codes for a tumor rejection antigen precursor, with the proviso that said isolated nucleic acid molecule does not code for a MAGE tumor rejection antigen precursor or a BAGE tumor rejection antigen precursor.

CLMS(18)

18. An isolated nucleic acid molecule consisting of nucleotides 51-467 of SEQ ID NO: 1.

CLMS(19)

19. An isolated mRNA molecule which is complementary to the isolated nucleic acid molecule of claim 16.

CLMS(20)

20. A host cell transfected with the isolated nucleic acid molecule of claim 16.

CLMS(21)

21. A host cell transfected with the isolated nucleic acid molecule of claim 17.

CLMS(22)

22. A host cell transfected with the isolated nucleic acid molecule of claim 18.

CLMS(23)

23. An expression vector comprising the isolated nucleic acid molecule of claim 16 operably linked to a promoter.

CLMS(24)

24. An expression vector comprising the isolated nucleic acid molecule of claim 17 operably linked to a promoter.

CLMS(25)

25. An expression vector comprising the isolated nucleic acid molecule of claim 18 operably linked to a promoter.

CLMS(26)

26. The host cell of claim 20, wherein said host cell is a mammalian cell which expresses HLA-Cw6.

CLMS(27)

27. The host cell of claim 21, wherein said host cell is a mammalian cell which expresses HLA-Cw6.

CLMS(28)

28. The host cell of claim 22, wherein said host cell is a mammalian cell which expresses HLA-Cw6.

CLMS(29)

29. The expression vector of claim 23, further comprising a nucleic acid molecule which codes for HLA-Cw6.

CLMS(30)

30. The expression vector of claim 24, further comprising a nucleic acid molecule which codes for HLA-Cw6.

CLMS(31)

31. The expression vector of claim 25, further comprising a nucleic acid molecule which codes for HLA-Cw6.

CLMS(32)

32. Expression kit comprising a separate portion of each of
(i) the expression vector of claim 23, and
(ii) a nucleic acid molecule which encodes HLA-Cw6.

CLMS(33)

33. Expression kit comprising a separate portion of each of
(i) the expression vector of claim 24, and,
(ii) a nucleic acid molecule which encodes HLA-Cw6.

CLMS(34)

34. Expression kit comprising
(i) the expression vector of claim 25, and
(ii) a nucleic acid molecule, which encodes HLA-Cw6.

CLMS(35)

35. The method of claim 2, wherein said expression product is a GAGE tumor rejection antigen precursor.

CLMS(36)

36. The method of claim 35, wherein said agent is an antibody.

CLMS(37)

37. Method for screening for a disorder characterized by expression of a tumor rejection antigen encoded by a cDNA molecule comprising nucleotides 51-476 of SEQ ID NO: 1, comprising contacting a cDNA or mRNA molecule containing sample from a subject with a nucleic acid hybridization probe which hybridizes to a cDNA molecule comprising nucleotides 51-476 of SEQ ID NO: 1, and determining binding of said hybridization probe to said

cDNA or mRNA molecules as an indication of possible presence of said disorder in said subje

US PAT NO: 5,587,289 [IMAGE AVAILABLE] L2: 8 of 13

CLAIMS:

CLMS(1)

We claim:

1. Isolated nucleic acid molecule which encodes a **MAGE**-Xp tumor rejection antigen precursor or is complementary to an isolated nucleic acid molecule which encodes a **MAGE**-Xp tumor rejection antigen precursor, wherein said isolated nucleic acid molecule (i) is not SEQ ID NO: 1, and (ii) hybridizes to at least one isolated nucleic acid molecule consisting of SEQ ID NO: 2, SEQ ID NO: 3, and SEQ ID NO: 4, under stringent conditions.

CLMS(2)

2. Isolated nucleic acid molecule selected from the group consisting of the isolated nucleic acid molecule consisting of the nucleotide sequence of SEQ ID NO: 1, the isolated nucleic acid molecule consisting of the nucleotide sequence of SEQ ID NO: 2, and the isolated nucleic acid molecule consisting of the nucleotide sequence of SEQ ID NO: 3.

CLMS(3)

3. The isolated nucleic acid molecule of claim 2, consisting of SEQ ID NO: 2.

CLMS(4)

4. The isolated nucleic acid molecule of claim 2, consisting of SEQ ID NO: 3.

CLMS(5)

5. The isolated nucleic acid molecule of claim 2, consisting of SEQ ID NO: 4.

CLMS(6)

6. Expression vector comprising the isolated nucleic acid molecule of claim 2, operably linked to a promoter.

CLMS(7)

7. Eukaryotic cell line transfected with the isolated nucleic acid molecule of claim 2.

CLMS(8)

8. Prokaryotic cell strain transformed with the isolated nucleic acid molecule of claim 2.

CLMS(9)

9. Method for identifying human X chromosome in a sample comprising contacting said sample with the isolated nucleic acid molecule of claim 1 under condition favoring hybridization of said isolated nucleic acid molecule to said X chromosome, and determining hybridization as a determination of said human X chromosome.

CLMS(10)

10. Isolated nucleic [redacted]d molecule selected from the g[redacted]p consisting of SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, and SEQ ID NO: 10.

CLMS(11)

11. Kit useful in a polymerase chain reaction based assay, comprising one of:
(i) SEQ ID NO: 5 and SEQ ID NO: 6,
(ii) SEQ ID NO: 7 and SEQ ID NO: 8, and
(iii) SEQ ID NO: 9 and SEQ ID NO: 10.

CLMS(12)

12. Method for determining transcription of a **MAGE**-Xp gene in a sample, comprising contacting said sample with at least one of (i) SEQ ID NO: 5 and SEQ ID NO: 6, (ii) SEQ ID NO: 7 and SEQ ID NO: 8, and (iii) SEQ ID NO: 9 and SEQ ID NO: 10, under conditions favoring hybridization of (i) (ii) or (iii) to mRNA or cDNA of a **MAGE**-Xp gene, carrying out polymerase chain reaction and determining an extension product of said polymerase chain reaction to determine transcription of said **MAGE**-Xp gene in said sample.

US PAT NO: 5,571,711 [IMAGE AVAILABLE] L2: 9 of 13

CLAIMS:

CLMS(1)

We claim:

1. An isolated nucleic acid molecule which codes for a BAGE, tumor rejection antigen precursor consisting of the nucleotide sequence set forth in SEQ ID NO: 1.

CLMS(2)

2. An isolated nucleic acid molecule which hybridizes, under stringent conditions, to the nucleotide sequence set forth in SEQ ID No: 1, wherein said isolated nucleic acid molecule consists of a nucleotide sequence which codes for a tumor rejection antigen precursor and said isolated nucleic acid does not code for a **MAGE** tumor rejection antigen precursor.

CLMS(3)

3. An isolated mRNA molecule which is complementary to the nucleic acid molecule of claim 2.

CLMS(4)

4. An expression vector comprising the isolated nucleic acid molecule of claim 1 operably linked to a promoter.

CLMS(5)

5. An expression vector comprising the isolated nucleic acid molecule of claim 2 operably linked to a promoter.

CLMS(6)

6. A host cell transfected with the expression vector of claim 4.

CLMS(7)

7. A host cell transfected with the expression vector of claim 5.

CLMS(8)

8. The host cell of claim 6, wherein said host cell is a mammalian cell which expresses HLA-C clone 10.

CLMS(9)

9. The host cell of claim 7, wherein said host cell is a mammalian cell which expresses HLA-C clone 10.

CLMS(10)

10. Expression kit comprising each of (i) the isolated nucleic acid molecule of claim 1, and (ii) separate from (i), a nucleic acid molecule which codes for HLA-C clone 10.

CLMS(11)

11. Expression kit comprising each of (i) the isolated nucleic acid molecule of claim 2, and (ii) separate from (i), a nucleic acid molecule which codes for HLA-C clone 10.

US PAT NO: 5,541,104 [IMAGE AVAILABLE] L2: 10 of 13

CLAIMS:

CLMS(1)

We claim:

1. Monoclonal antibody which specifically binds to tumor rejection antigen precursor **MAGE-1**.

CLMS(2)

2. The monoclonal antibody of claim 1, designated MA454 produced by the hybridoma having A.T.C.C. Accession Number HB 11540.

CLMS(3)

3. Hybridoma cell line which produces the monoclonal antibody of claim 1.

CLMS(4)

4. The hybridoma cell line of claim 3, designated A.T.C.C. Accession No. HB 11540 and wherein said monoclonal antibody is MA454.

US PAT NO: 5,512,444 [IMAGE AVAILABLE] L2: 11 of 13

CLAIMS:

CLMS(1)

What is claimed is:

1. Method for screening for bladder cancer in a subject, comprising assaying a bladder tissue sample from a subject to determine expression of mRNA of at least one member of the group of genes encoding **MAGE-1**, **MAGE-2**, **MAGE-3** and **MAGE-4** tumor rejection antigen precursors, wherein expression of said mRNA is an indication of possibility of bladder cancer in said subject.

CLMS(2)

2. The method of clai[redacted], comprising determining said [redacted]A expression via a nucleic acid amplification assay.

CLMS(3)

3. The method of claim 2, wherein said amplification assay is polymerase chain reaction.

CLMS(4)

4. The method of claim 3, comprising carrying out polymerase chain reaction with a pair of primers selected from the group consisting of: (i) SEQ ID NO: 1 and SEQ ID NO: 2; (ii) SEQ ID NO: 3 and SEQ ID NO: 4; (iii) SEQ ID NO: 5 and SEQ ID NO: 6; (iv) SEQ ID NO: 7 and SEQ ID NO: 8, and (v) SEQ ID NO: 9 and SEQ ID NO: 10.

CLMS(5)

5. Method for screening for bladder cancer in a subject, comprising assaying a bladder tissue sample from a subject to determine presence of at least one member of the group of **MAGE-1**, **MAGE**-2, **MAGE**-3 and **MAGE**-4 tumor rejection antigen precursors in said sample is an indication of possibility of bladder cancer in said subject.

CLMS(6)

6. The method of claim 5, comprising determining saw at least one of said tumor rejections antigen precursors in an immunoassay.

CLMS(7)

7. Method for monitoring status of a bladder cancer comprising:
(i) assaying a sample of bladder cancer cells taken from a subject with bladder cancer to determine expression of mRNA for at least one member of the group of genes encoding **MAGE-1**, **MAGE**-2 **MAGE**-3 and **MAGE**-4 tumor rejections antigen precursors, to determine a value, wherein said value is the level of mRNA expression in said sample and
(ii) comparing the value determined in (i) to a value determined previously for the member or members of the group of genes encoding **MAGE-1**, **MAGE**-2, **MAGE**-3 and **MAGE**-4 tumor rejection antigen precursors obtained the same way the value in (i) was determined, wherein a change in the value obtained in (i) as compared to the value determined previously shows a change in status of said bladder cancer.

US PAT NO: 5,512,437 [IMAGE AVAILABLE] L2: 12 of 13

CLAIMS:

CLMS(1)

We claim:

1. Method for screening for possible presence of cancer, wherein said cancer is selected from the group consisting of head squamous cell carcinoma, neck squamous cell carcinoma, and prostate carcinoma, comprising assaying a tissue sample taken from the head, neck or prostate gland of a subject believed to have a head squamous cell carcinoma, a neck squamous cell carcinoma or a prostate carcinoma, and determining expression of mRNA for a **MAGE**-3 gene, as a determination of possible presence of said cancer in said subject.

CLMS(2)

2. The method of claim 1, comprising determining said expression by in vitro amplification of said mRNA.

CLMS(3)

3. The method of claim 2, wherein said in vitro amplification is polymerase chain reaction.

CLMS(4)

4. The method of claim 1, comprising determining expression of said mRNA with a labelled nucleodtide probe which specifically hybridizes to said mRNA.

CLMS(5)

5. The method of claim 3, further comprising carrying out said polymerase chain reaction with at least one primer selected from the group consisting of SEQ ID NO:1 and SEQ ID NO:2.

CLMS(6)

6. The method of claim 4, wherein said labelled nucleotide probe is a labelled nucleic acid molecule selected from the group consisting of SEQ ID NO:1 and SEQ ID NO: 2.

CLMS(7)

7. Method for screening for possible presence of cancer, wherein said cancer is selected from the group consisting of head squamous cell carcinoma, neck squamous cell carcinoma, and prostate cancer, comprising assaying a tissue sample taken from the head, neck or prostate gland of a subject believed to have a head squamous cell carcinoma, a neck squamous cell carcinoma or a prostate carcinoma and determining expression of **MAGE**-3 protein, as a determination of possible presence of said cancer in said subject.

CLMS(8)

8. The method of 7, comprising determining expression of **MAGE**-3 protein by immunoassay.

CLMS(9)

9. Isolated nucleic acid molecule selected from the group consisting of SEQ ID NO:1, and SEQ ID NO:2.

CLMS(10)

10. Kit useful in determining expression of mRNA for **MAGE**-3 gene in a cell sample, comprising separated portions of each of SEQ ID NO:1 and SEQ ID NO:2, and a means for containing both of said separate nucleic acid molecules.

CLMS(11)

11. The kit of claim 10, further comprising a separate portion of a polymerase.

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